

```

      10      20      30      40      50      60
SEQIDNO:1 5789228 ATGATAAACGTTGCAACGGGACAGCAGACCCCAATACACCTCTATCGAGTAAACGCTTC
SEQIDNO:45 09/914543 atga-----gcaa--gaaaa-aggtagtcatcgtaacctatc--ttaacaa--tc

      70      80      90     100     110     120
SEQIDNO:1 5789228 GGCTTTTCAGACACCCGAAGTACGTTCTTCACGGCCTATCGAGTAGCAACTGGGAGCA CA
SEQIDNO:45 09/914543 ---ctttcagtagcggc--aa--ta--tatt-----t--gtagaaa--agtagta

      130     140     150     160     170     180
SEQIDNO:1 5789228 TCCATCTCCAGATCAAGAGCCTTGGCTTCAATCCGATAGGCTTCCTCTCGTAGCCCACT
SEQIDNO:45 09/914543 tagctctgagga--caag--tcaactttcaa--ata--cct--ca--t

      190     200     210     220     230     240
SEQIDNO:1 5789228 GACTAAACCGGGGACGATGCCAAACGGGATATGACTACGGCAAGAACCCAGACCTCCAGG
SEQIDNO:45 09/914543 c--taacacc--ac--ccaaa--caac--acttt--ccacta--cca--agg

      250     260     270     280     290     300
SEQIDNO:1 5789228 GTCTTGACAGCGTCCAGATATCGCAAAATATATCAAGANCGCTGGNAGCCTGGCCATAT
SEQIDNO:45 09/914543 ttct--ca-----agattc--gataccctgat--gaagg--tg--tag--tggccag--

      310     320     330     340     350     360
SEQIDNO:1 5789228 TCCAGCTCTCCGACTACCCACAGAAATAGGATGCAACTTCATAGAACCCCTATGGGACACCG
SEQIDNO:45 09/914543 --gagctcct--act-----gataaggatgg-----tga-----tggga--acc

      370     380     390     400     410     420
SEQIDNO:1 5789228 AACCCTTCTCCGAGCAAGCACTACATAAACACCTGGCTTGAAGTCCGCCAGAGGTTCCGC
SEQIDNO:45 09/914543 agaa--ttct--a--caatga--ataaac--ctatg--gaa--ca--ttotta

      430     440     450     460     470     480
SEQIDNO:1 5789228 AAC-TACTGGAACCTTATCGGGCCGACCTTCAGAACCAACCCACAGCTCAAGCCCGG
SEQIDNO:45 09/914543 atgctactgga--ttt--gcaga--gataga--cgtac--attttaa--caagc

      490     500     510     520     530     540
SEQIDNO:1 5789228 AACTGCGCGCTTCACTGACCGGAAGTGGGGCCACGTTGGGAATGGGCAACAGCGCACCGGA
SEQIDNO:45 09/914543 g--gggtccttcaact--acgtc--caacaactt--ga

      550     560     570     580     590     600
SEQIDNO:1 5789228 CTGGAACCTCCCGCTGAGAGGATAGGAAGGCAATTCTGGAGGTTCGCCACACATGGGT
SEQIDNO:45 09/914543 c--aacattgtct--tgag--gatatag--aagt--aatt--ggggc--atgg--

      610     620     630     640     650     660
SEQIDNO:1 5789228 TATATTCTGTGAGGGAAACCCAGTTCAACCAACCCCGACATAGACGGTAGCTCAAGTGGG
SEQIDNO:45 09/914543 --ata-----ccccgaata--tctat--tgg--

      670     680     690     700     710     720
SEQIDNO:1 5789228 CCACAAACGCGGTGGGGCGGAAACCTTATGGGTGTATAGGAAGTACCAGTTTAACTTCG
SEQIDNO:45 09/914543 --a--aac--aaagcc--atgg--aaatgg--aaactag--

      730     740     750     760     770     780

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SEQIDNO:1 5789228
 SEQIDNO:45 09/914543

790 800 810 820 830 840

SEQIDNO:1 5789228
 SEQIDNO:45 09/914543

850 860 870 880 890 900

SEQIDNO:1 5789228
 SEQIDNO:45 09/914543

910 920 930 940 950 960

SEQIDNO:1 5789228
 SEQIDNO:45 09/914543

970 980 990 1000 1010 1020

SEQIDNO:1 5789228
 SEQIDNO:45 09/914543

1030 1040 1050 1060 1070 1080

SEQIDNO:1 5789228
 SEQIDNO:45 09/914543

1090 1100 1110 1120 1130 1140

SEQIDNO:1 5789228
 SEQIDNO:45 09/914543

1150 1160 1170 1180 1190 1200

SEQIDNO:1 5789228
 SEQIDNO:45 09/914543

1210 1220 1230 1240 1250 1260

SEQIDNO:1 5789228
 SEQIDNO:45 09/914543

1270 1280 1290 1300 1310 1320

SEQIDNO:1 5789228
 SEQIDNO:45 09/914543

1330 1340 1350 1360 1370 1380

SEQIDNO:1 5789228
 SEQIDNO:45 09/914543

1390 1400 1410 1420 1430 1440

SEQIDNO:1 5789228
 SEQIDNO:45 09/914543

1450 1460 1470 1480 1490 1500

SEQIDNO:1 5789228
 SEQIDNO:45 09/914543

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      1510      1520      1530      1540      1550      1560
SEQIDNO:1 5789228 GCTCAAGGTTACAAACCTCTGGAACATCAACATGCATCCGAAGTATAACACAATGGGATA
SEQIDNO:45 09/914543 g---ag--tt-----tggaagccaa--gca--c-----taacttc---gccca

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      1570      1580      1590      1600      1610      1620
SEQIDNO:1 5789228 CCCGAGGTCATATAACGGCCCAAGCCTTGGGCAACCAAGCCAATAAACGCTCCGAACCT
SEQIDNO:45 09/914543 cctagag-----t--gg-----tggatca--caacaa--taa--caot---aac--

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      1630      1640      1650      1660
SEQIDNO:1 5789228 CGTGCTCCCGATAAAGCTCTCCAGCTTCGGAGGATACTTCGTTCA
SEQIDNO:45 09/914543 c---ctctagatagac--ctc-----tt-----at--ttcch--a

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